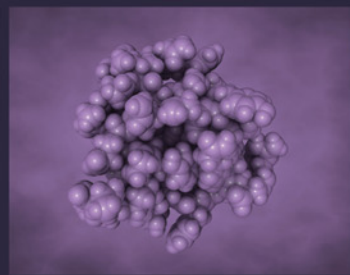


Unlocking Sirtuins

Cellular Biology to Translational Research



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Pranav Kumar Prabhakar
Sumel Ashique





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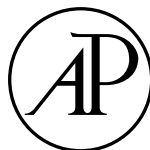
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ACADEMIC PRESS

An imprint of Elsevier

Academic Press is an imprint of Elsevier
125 London Wall, London EC2Y 5AS, United Kingdom
50 Hampshire Street, 5th Floor, Cambridge, MA 02139, United States

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ISBN: 978-0-443-45380-9

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Publisher: Megan Ball
Acquisitions Editor: Michelle Fisher
Editorial Project Manager: Ashavari Bhattacharya
Production Project Manager: Sathyavani Deivasigamani
Cover Designer: Venkatraman Gopalakrishan

Typeset by MPS Limited, Chennai, India





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The role of sirtuins in cancer progression

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10.1 Introduction

Sirtuins represent a highly conserved family of nicotinamide adenine dinucleotide (NAD⁺)-dependent deacetylases that have emerged as pivotal regulators at the intersection of cellular metabolism, epigenetic regulation, and cancer biology. First identified as the mammalian orthologs of yeast Silent Information Regulator 2 (Sir2), the seven mammalian sirtuins (SIRT1–SIRT7) share a conserved catalytic core domain of approximately 275 amino acids yet exhibit remarkable functional diversity through distinct subcellular localizations, enzymatic activities, and substrate specificities. This evolutionary conservation from bacteria to mammals highlights their fundamental importance in cellular homeostasis and organismal survival. In the context of cancer, sirtuins have garnered substantial attention over the past two decades not merely as metabolic sensors, but as master regulators whose dysregulation profoundly influences tumor initiation, progression, and therapeutic response (Chang & Guarente, 2014; Hong & Lin, 2021; Sanders et al., 2010; Sun & Dang, 2020; Wang et al., 2020; Yu et al., 2024). The structural organization and subcellular compartmentalization of sirtuins confer their functional specialization. SIRT1, SIRT6, and SIRT7 predominantly localize to the nucleus, where they orchestrate chromatin remodeling and gene transcription regulation through histone deacetylation (Chang & Guarente, 2014). SIRT1, the most extensively studied family member, shuttles dynamically between the nucleus and cytoplasm in response to specific cellular stimuli, enabling it to coordinate diverse biological processes ranging from DNA damage repair to metabolic adaptation (Hashemi et al., 2025). SIRT2 functions primarily in the cytosol but translocates to the nucleus during the G2/M phase of the cell cycle to deacetylate histone H4 at lysine 16 (H4K16ac), thereby influencing mitotic progression and genomic stability. The mitochondrial sirtuins—SIRT3, SIRT4, and SIRT5—constitute the largest subgroup and serve as critical guardians of mitochondrial metabolic homeostasis, regulating oxidative phosphorylation (OXPHOS), reactive oxygen species (ROS) production, and nutrient catabolism. SIRT7 resides predominantly in the nucleolus, where it regulates ribosomal RNA transcription through H3K18 deacetylation, thereby controlling protein synthesis and cellular growth (Hamaidi & Kim, 2022; Min and Gao, 2019; Sun & Dang, 2020; Wang et al., 2021).